Amendments to the Specification:

Please replace the paragraph beginning at page24, line 19, with the following amended paragraph:

To determine the nucleotide sequence of the NES1 cDNA, double-stranded sequencing was performed initially using two primers corresponding to the SP6 promoter (5'-CCG-CAG-ATT-TAG-GTG-ACA-C) (SEQ ID NO:3) and the T7 promoter (5'-GGC-CTC-TAA-TAC-GAC-TCA-C) (SEQ ID NO:4). Further full-length cDNA sequencing (in both directions) utilized two primers corresponding to the vector pGAD10 (i.e., the vector used for the second 76N cDNA library screen described above); these primers were of the following sequence: 5'-TAC-CAC-TAC-AAT-GGA-TG-3' (SEQ ID NO:5) (upstream primer) and 5'-GTT-GAA-GTG-AAC-TTG-CGG-GC-3' (SEQ ID NO:6) (downstream primer), as well as 12 NES1 sense primers (corresponding to nucleotides 6-22, 72-91, 128-145, 196-213, 344-36-, 484-500, 634-650, 723-739, 851-867, 998-1116, 1125-1141, and 1253-1269) and 10 NES1 antisense primers (corresponding to nucleotides 1392-1377, 1294-1277, 1201-1185, 1086-1069, 917-899, 307-789, 674-657, 516-488, 292-275, and 176-161). Comparison of the cDNA sequence to the GENBANK database revealed no exact match, indicating that NES1 was a novel gene. The nucleotide sequence revealed an open reading frame of 277 amino acids followed by a stop codon (Fig. 11; SEQ ID NO: 2). A polyadenylations signal (ATATAA) was observed near the 3' end of the cDNA, indicating that this represents the 3' untranslated region.